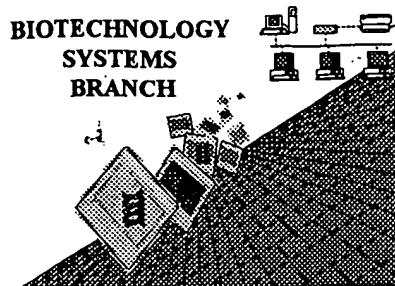


0570
0815



RAW SEQUENCE LISTING **ERROR REPORT**

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) detected errors when processing the following computer readable form:

Application Serial Number: 09/758,017
Source: OIPF
Date Processed by STIC: 8/17/2001

THE ATTACHED PRINTOUT EXPLAINS DETECTED ERRORS.

PLEASE FORWARD THIS INFORMATION TO THE APPLICANT BY EITHER:

- 1) INCLUDING A COPY OF THIS PRINTOUT IN YOUR NEXT COMMUNICATION TO THE APPLICANT, WITH A NOTICE TO COMPLY or,**
- 2) TELEPHONING APPLICANT AND FAXING A COPY OF THIS PRINTOUT, WITH A NOTICE TO COMPLY**

FOR CRF SUBMISSION QUESTIONS, PLEASE CONTACT MARK SPENCER, 703-308-4212.

FOR SEQUENCE RULES INTERPRETATION, PLEASE CONTACT ROBERT WAX, 703-308-4216.

PATENTIN 2.1 e-mail help: patin21help@uspto.gov or phone 703-306-4119 (R. Wax)

PATENTIN 3.0 e-mail help: patin3help@uspto.gov or phone 703-306-4119 (R. Wax)

TO REDUCE ERRORED SEQUENCE LISTINGS, PLEASE USE THE CHECKER VERSION 3.0 PROGRAM, ACCESSIBLE THROUGH THE U.S. PATENT AND TRADEMARK OFFICE WEBSITE. SEE BELOW:

Checker Version 3.0

The Checker Version 3.0 application is a state-of-the-art Windows based software program employing a logical and intuitive user-interface to check whether a sequence listing is in compliance with format and content rules. Checker Version 3.0 works for sequence listings generated for the original version of 37 CFR §§1.821 – 1.825 effective October 1, 1990 (old rules) and the revised version (new rules) effective July 1, 1998 as well as World Intellectual Property Organization (WIPO) Standard ST.25.

Checker Version 3.0 replaces the previous DOS-based version of Checker, and is Y2K-compliant. Checker allows public users to check sequence listings in Computer Readable form (CRF) before submitting them to the United States Patent and Trademark Office (USPTO). Use of Checker prior to filing the sequence listing is expected to result in fewer errored sequence listings, thus saving time and money.

Checker Version 3.0 can be down loaded from the USPTO website at the following address:

<http://www.uspto.gov/web/offices/pac/checker>

Raw Sequence Listing Error Summary

ERROR DETECTED

SUGGESTED CORRECTION

SERIAL NUMBER: 09/758,017

ATTN: NEW RULES CASES: PLEASE DISREGARD ENGLISH "ALPHA" HEADERS, WHICH WERE INSERTED BY PTO SOFTWARE

- 1 _____ Wrapped Nucleics
_____ Wrapped Aminos
The number/text at the end of each line "wrapped" down to the next line. This may occur if your file was retrieved in a word processor after creating it. Please adjust your right margin to .3; this will prevent "wrapping."
- 2 _____ Invalid Line Length
The rules require that a line not exceed 72 characters in length. This includes white spaces.
- 3 _____ Misaligned Amino
_____ Numbering
The numbering under each 5th amino acid is misaligned. Do not use tab codes between numbers; use space characters, instead.
- 4 _____ Non-ASCII
The submitted file was not saved in ASCII(DOS) text, as required by the Sequence Rules. Please ensure your subsequent submission is saved in ASCII text.
- 5 _____ Variable Length
Sequence(s) _____ contain n's or Xaa's representing more than one residue. Per Sequence Rules, each n or Xaa can only represent a single residue. Please present the maximum number of each residue having variable length and indicate in the <220>-<223> section that some may be missing.
- 6 _____ PatentIn 2.0
_____ "bug"
A "bug" in PatentIn version 2.0 has caused the <220>-<223> section to be missing from amino acid sequences(s) _____. Normally, PatentIn would automatically generate this section from the previously coded nucleic acid sequence. Please manually copy the relevant <220>-<223> section to the subsequent amino acid sequence. This applies to the mandatory <220>-<223> sections for Artificial or Unknown sequences.
- 7 _____ Skipped Sequences
_____ (OLD RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence:
(2) INFORMATION FOR SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
(i) SEQUENCE CHARACTERISTICS: (Do not insert any subheadings under this heading)
(xi) SEQUENCE DESCRIPTION:SEQ ID NO:X: (insert SEQ ID NO where "X" is shown)
This sequence is intentionally skipped

Please also adjust the "(ii) NUMBER OF SEQUENCES:" response to include the skipped sequences.
- 8 _____ Skipped Sequences
_____ (NEW RULES)
Sequence(s) _____ missing. If intentional, please insert the following lines for each skipped sequence.
<210> sequence id number
<400> sequence id number
000
- 9 _____ Use of n's or Xaa's
_____ (NEW RULES)
Use of n's and/or Xaa's have been detected in the Sequence Listing.
Per 1.823 of Sequence Rules, use of <220>-<223> is MANDATORY if n's or Xaa's are present.
In <220> to <223> section, please explain location of n or Xaa, and which residue n or Xaa represents.
- 10 _____ Invalid <213>
_____ Response
Per 1.823 of Sequence Rules, the only valid <213> responses are: Unknown, Artificial Sequence, or scientific name (Genus/species). <220>-<223> section is required when <213> response is Unknown or is Artificial Sequence
- 11 _____ Use of <220>
Sequence(s) _____ missing the <220> "Feature" and associated numeric identifiers and responses.
Use of <220> to <223> is MANDATORY if <213> "Organism" response is "Artificial Sequence" or "Unknown." Please explain source of genetic material in <220> to <223> section.
(See "Federal Register," 06/01/1998, Vol. 63, No. 104, pp. 29631-32) (Sec. 1.823 of Sequence Rules)
- 12 _____ PatentIn 2.0
_____ "bug"
Please do not use "Copy to Disk" function of PatentIn version 2.0. This causes a corrupted file, resulting in missing mandatory numeric identifiers and responses (as indicated on raw sequence listing). Instead, please use "File Manager" or any other manual means to copy file to floppy disk.
- 13 _____ Misuse of n
n can only be used to represent a single nucleotide in a nucleic acid sequence. N is not used to represent any value not specifically a nucleotide.

OIPE

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/758,017

DATE: 08/17/2001

TIME: 12:01:30

Input Set : A:\U0132093.app

Output Set: N:\CRF3\08162001\I758017.raw

pp1-2

**Does Not Comply
Corrected Diskette Needed**

3 <110> APPLICANT: Lanes, Olav
 4 Willasen, Nils Peder
 5 Guddal, Per Henrik
 6 Gjellesvik, Dag Rune
 8 <120> TITLE OF INVENTION: Cod uracil-DNA glycosylase, gene coding therefore,
 9 recombinant DNA containing said gene or operative parts
 10 thereof, a method for preparing said protein and the
 11 use of said protein or said operative pa
 13 <130> FILE REFERENCE: U013209-3
 15 <140> CURRENT APPLICATION NUMBER: 09/758,017
 16 <141> CURRENT FILING DATE: 2001-01-10
 18 <150> PRIOR APPLICATION NUMBER: 2000 5428
 19 <151> PRIOR FILING DATE: 2000-10-27
 21 <150> PRIOR APPLICATION NUMBER: 2000 0163
 22 <151> PRIOR FILING DATE: 2000-01-12
 24 <160> NUMBER OF SEQ ID NOS: 19
 26 <170> SOFTWARE: PatentIn Ver. 2.0

ERRORED SEQUENCES

131 <210> SEQ ID NO: 2
 132 <211> LENGTH: 301
 133 <212> TYPE: PRT
 134 <213> ORGANISM: Gadus morhua
 136 <400> SEQUENCE: 2
 137 Met Leu Phe Lys Leu Gly Leu Cys Gln Arg Cys Ile Ser Ser Asn Arg
 138 1 5 10 15
 E--> 140 Xaa Leu Pro Gly Leu Leu Ile Pro Gln Thr Leu Cys Phe Ser Lys Leu
 141 20 25 30
 143 Met Lys Ile Thr Pro Lys Lys Leu Arg Ser Ser Asn Val Glu Gln Lys
 144 35 40 45
 146 Thr Ser Ser Pro Gln Leu Ser Val Glu Gln Leu Glu Arg Met Ala Lys
 147 50 55 60
 149 Asn Lys Lys Ala Ala Leu Asp Lys Ile Arg Ala Lys Ala Thr Pro Ala
 150 65 70 75 80
 152 Gly Phe Gly Glu Thr Trp Arg Arg Glu Leu Ala Ala Glu Phe Glu Lys
 153 85 90 95
 155 Pro Tyr Phe Lys Gln Leu Met Ser Phe Val Ala Asp Glu Arg Ser Arg
 156 100 105 110
 158 His Thr Val Tyr Pro Pro Ala Asp Gln Val Tyr Ser Ser Thr Glu Met
 159 115 120 125
 161 Cys Asp Ile Gln Asp Val Lys Val Val Ile Leu Gly Gln Asp Pro Tyr
 162 130 135 140
 164 His Gly Pro Asn Gln Ala His Gly Leu Cys Phe Ser Val Gln Lys Pro
 165 145 150 155 160
 167 Val Pro Pro Pro Pro Ser Leu Val Asn Ile Tyr Lys Glu Leu Cys Thr

→ see
 item 9
 on Enn
 summary
 sheet

RAW SEQUENCE LISTING

PATENT APPLICATION: US/09/758,017

DATE: 08/17/2001

TIME: 12:01:31

Input Set : A:\U0132093.app

Output Set: N:\CRF3\08162001\I758017.raw

168		165		170		175
170	Asp	Ile	Asp	Gly	Phe	Lys
171				180		185
173	Ala	Lys	Gln	Gly	Val	Leu
174				195		200
176	His	Gln	Ala	Asn	Ser	His
177				210		215
179	Ala	Val	Ile	Lys	Trp	Leu
180	225			230		235
182	Leu	Trp	Gly	Ser	Tyr	Ala
183				245		250
185	Arg	His	His	Val	Leu	Gln
186				260		265
188	Arg	Gly	Phe	Leu	Gly	Cys
189				275		280
191	Lys	Leu	Ser	Gly	Thr	Glu
192				290		295

Use of n and/or Xaa has been detected in the Sequence Listing.
 Review the Sequence Listing to insure a corresponding
 explanation is presented in the <220> to <223> fields of
 each sequence using n or Xaa.

PSI

VERIFICATION SUMMARY

PATENT APPLICATION: US/09/758,017

DATE: 08/17/2001

TIME: 12:01:32

Input Set : A:\U0132093.app

Output Set: N:\CRF3\08162001\I758017.raw

L:43 M:258 W: Mandatory Feature missing, <223> not found for SEQ ID#:1

L:43 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:1

L:140 M:340 E: (46) "n" or "Xaa" used: Feature required, for SEQ ID#:2